

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: ARMITAGE, RICHARD  
FANSLOW, WILLIAM  
SPRIGGS, MELANIE  
SRINIVASAN, SUBHASHINI  
GIBSON, MARYLOU
- (ii) TITLE OF INVENTION: NOVEL CYTOKINE
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: IMMUNEX CORPORATION
  - (B) STREET: 51 UNIVERSITY STREET
  - (C) CITY: SEATTLE
  - (D) STATE: WASHINGTON
  - (E) COUNTRY: USA
  - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: Apple Macintosh
  - (C) OPERATING SYSTEM: Apple Operating System 7.1
  - (D) SOFTWARE: Microsoft Word for Apple, version 5.1a
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 07/969,703
  - (B) FILING DATE: October 23, 1992
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 07/805,723
  - (B) FILING DATE: December 5, 1991
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 07/783,707
  - (B) FILING DATE: October 25, 1991
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Perkins, Patricia A.
  - (B) REGISTRATION NUMBER: 34,693
  - (C) REFERENCE/DOCKET NUMBER: 2802-C
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 2065870430
  - (B) TELEFAX: 2065870606

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 783 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: MOUSE

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40-L

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG ATA GAA ACA TAC AGC CAA CCT TCC CCC AGA TCC GTG GCA ACT GGA  
48  
Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly  
1 5 10 15  
CTT CCA GCG AGC ATG AAG ATT TTT ATG TAT TTA CTT ACT GTT TTC CTT  
96  
Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu  
20 25 30  
ATC ACC CAA ATG ATT GGA TCT GTG CTT TTT GCT GTG TAT CTT CAT AGA  
144  
Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg  
35 40 45  
AGA TTG GAT AAG GTC GAA GAG GAA GTA AAC CTT CAT GAA GAT TTT GTA  
192  
Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val  
50 55 60  
TTC ATA AAA AAG CTA AAG AGA TGC AAC AAA GGA GAA GGA TCT TTA TCC  
240  
Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser  
65 70 75 80  
TTG CTG AAC TGT GAG GAG ATG AGA AGG CAA TTT GAA GAC CTT GTC AAG  
288  
Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys  
85 90 95

GAT ATA ACG TTA AAC AAA GAA GAG AAA AAA GAA AAC AGC TTT GAA ATG  
 336  
 Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met  
 100 105 110

CAA AGA GGT GAT GAG GAT CCT CAA ATT GCA GCA CAC GTT GTA AGC GAA  
 384  
 Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu  
 115 120 125

GCC AAC AGT AAT GCA GCA TCC GTT CTA CAG TGG GCC AAG AAA GGA TAT  
 432  
 Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr  
 130 135 140

TAT ACC ATG AAA AGC AAC TTG GTA ATG CTT GAA AAT GGG AAA CAG CTG  
 480  
 Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu  
 145 150 155 160

ACG GTT AAA AGA GAA GGA CTC TAT TAT GTC TAC ACT CAA GTC ACC TTC  
 528  
 Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe  
 165 170 175

TGC TCT AAT CGG GAG CCT TCG AGT CAA CGC CCA TTC ATC GTC GGC CTC  
 576  
 Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu  
 180 185 190

TGG CTG AAG CCC AGC AGT GGA TCT GAG AGA ATC TTA CTC AAG GCG GCA  
 624  
 Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala  
 195 200 205

AAT ACC CAC AGT TCC TCC CAG CTT TGC GAG CAG CAG TCT GTT CAC TTG  
 672  
 Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu  
 210 215 220

GGC GGA GTG TTT GAA TTA CAA GCT GGT GCT TCT GTG TTT GTC AAC GTG  
 720  
 Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val  
 225 230 235 240

ACT GAA GCA AGC CAA GTG ATC CAC AGA GTT GGC TTC TCA TCT TTT GGC  
 768  
 Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly  
 245 250 255

TTA CTC AAA CTC TGA  
 783  
 Leu Leu Lys Leu  
 260

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 260 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly
 1           5           10           15
Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
          20           25           30
Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg
          35           40           45
Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val
          50           55           60
Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser
          65           70           75           80
Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys
          85           90           95
Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met
          100          105          110
Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu
          115          120          125
Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr
          130          135          140
Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu
          145          150          155          160
Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe
          165          170          175
Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu
          180          185          190
Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala
          195          200          205
Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu
          210          215          220
Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val
          225          230          235          240
Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly
          245          250          255

Leu Leu Lys Leu

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## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 740 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:

(B) CLONE: IgG1 Fc

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGGTACCGCT AGCGTCGACA GGCCTAGGAT ATCGATACGT AGAGCCCAGA TCTTGTGACA  
60

AAACTCACAC ATGCCCACCG TGCCAGCAC CTGAACTCCT GGGGGGACCG TCAGTCTTCC  
120

TCTTCCCCC AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG GTCACATGCG  
180

TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT CAACTGGTAC GTGGACGGCG  
240

TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA GTACAACAGC ACGTACCGGG  
300

TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAGGAC TACAAGTGCA  
360

AGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TGCAGAAAAC CATCTCCAA GCCAAAGGGC  
420

AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCATCCCG GGATGAGCTG ACCAAGAACC  
480

AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTATCCAG GCACATCGCC GTGGAGTGGG  
540

AGAGCAATGG GCAGCCGGAG AACAACTACA AGACCACGCC TCCCGTGCTG GACTCCGACG  
600

GCTCCTTCTT CCTCTACAGC AAGCTACCG TGGACAAGAG CAGGTGGCAG CAGGGGAACG  
660

TCTTCTCATG CTCCGTGATG CATGAGGCTC TGCACAACCA CTACACGCAG AAGAGCCTCT  
720

CCCTGTCTCC GGGTAAATGA  
740

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 519 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: HUMAN

(vii) IMMEDIATE SOURCE:  
    (B) CLONE: CD40 EXTRACELLULAR REGION

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGAACCACC CACTGCATGC AGAGAAAAAC AGTACCTAAT AAACAGTCAG TGCTGTTCTT  
60

TGTGCCAGCC AGGACAGAAA CTGGTGAGTG ACTGCACAGA GTTCACTGAA ACGGAATGCC  
120

TTCCTTGCGG TGAAAGCGAA TTCCTAGACA CCTGGAACAG AGAGACACAC TGCCACCAGC  
180

ACAAATACTG CGACCCCAAC CTAGGGCTTC GGGTCCAGCA GAAGGGCACC TCAGAAACAG  
240

ACACCATCTG CACCTGTGAA GAAGGCTGGC ACTGTACGAG TGAGGCCTGT GAGAGCTGTG  
300

TCCTGCACCG CTCATGCTCG CCCGGCTTTG GGGTCAAGCA GATTGCTACA GGGGTTTCTG  
360

ATACCATCTG CGAGCCCTGC CCAGTCGGCT TCTTCTCCAA TGTGTCATCT GCTTTCGAAA  
420

AATGTCACCC TTGGACAAGC TGTGAGACCA AAGACCTGGT TGTGCAACAG GCAGGCACAA  
480

ACAAGACTGA TGTTGTCTGT GGTCCCCAGG ATCGGCTGA  
519

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PCR PRIMER
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: CD40 5' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGTCGACCA CCATGGTTCG TCTGCC  
26

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PCR PRIMER
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: CD40 3' PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGTCGACGT CTAGAGCCGA TCCTGGGG  
28

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: CD40 3' DOWNSTREAM PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACAAGATCTG GGCTCTACGT ACTCAGCCGA TCCTGGGGAC  
40

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PENTAPEPTIDE

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Tyr Val Gly Pro Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:

(B) CLONE: HUMAN IGG1/FC 5' PRIMER



Year	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020
Population	1,000	1,500	2,000	2,500	3,000	3,500	4,000	4,500	5,000	5,500	6,000	6,500	7,000
Area (sq. mi.)	100	100	100	100	100	100	100	100	100	100	100	100	100
Population Density	10	15	20	25	30	35	40	45	50	55	60	65	70

TATTAATCAT TCAGTAGGGC CCAGATCTTG TGACAAAACT CAC  
43

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 38 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: PCR PRIMER

(vii) IMMEDIATE SOURCE:  
(B) CLONE: HUMAN IGG1/FC 3' DOWNSTREAM PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCAGCTTAA CTAGTTCATT TACCCGGAGA CAGGGAGA  
38

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 840 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:  
(B) CLONE: CD40-L

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 46..831
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:



Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser  
 165 170 175  
 AAT CGG GAA GCT TCG AGT CAA GCT CCA TTT ATA GCC AGC CTC TGC CTA  
 630  
 Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu  
 180 185 190 195  
 AAG TCC CCC GGT AGA TTC GAG AGA ATC TTA CTC AGA GCT GCA AAT ACC  
 678  
 Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr  
 200 205 210  
 CAC AGT TCC GCC AAA CCT TGC GGG CAA CAA TCC ATT CAC TTG GGA GGA  
 726  
 His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His Leu Gly Gly  
 215 220 225  
 GTA TTT GAA TTG CAA CCA GGT GCT TCG GTG TTT GTC AAT GTG ACT GAT  
 774  
 Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp  
 230 235 240  
 CCA AGC CAA GTG AGC CAT GGC ACT GGC TTC ACG TCC TTT GGC TTA CTC  
 822  
 Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu  
 245 250 255  
 AAA CTC TGAACAGTGT CA  
 840  
 Lys Leu  
 260

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 261 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly  
 1 5 10 15  
 Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu  
 20 25 30  
 Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg  
 35 40 45  
 Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val  
 50 55 60  
 Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser

65

70

75

80

Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys  
                             85                            90                            95  
 Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu  
                             100                            105                            110  
 Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser  
                             115                            120                            125  
 Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly  
                             130                            135                            140  
 Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln  
                             145                            150                            155                            160  
 Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr  
                             165                            170                            175  
 Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser  
                             180                            185                            190  
 Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala  
                             195                            200                            205  
 Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser Ile His  
                             210                            215                            220  
 Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn  
                             225                            230                            235                            240  
 Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe  
                             245                            250                            255  
 Gly Leu Leu Lys Leu  
                             260

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:



[illegible]

TAT 48	ATG	TTC	CAT	GTT	TCT	TTT	AGA	TAT	ATC	TTT	GGA	ATT	CCT	CCA	CTG
	Met -25	Phe	His	Val	Ser	Phe -20	Arg	Tyr	Ile	Phe	Gly -15	Ile	Pro	Pro	Leu
ATC 96	CTT	GTT	CTG	CTG	CCT	GTC	ACT	AGC	TCT	GAC	TAC	AAA	GAT	GAC	GAT
Ile -10	Leu	Val	Leu	Leu	Pro -5	Val	Thr	Ser	Ser	Asp 1	Tyr	Lys	Asp	Asp 5	Asp
GAT 144	AAA	AGA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA
Asp	Lys	Arg	Ser 10	Cys	Asp	Lys	Thr	His 15	Thr	Cys	Pro	Pro	Cys 20	Pro	Ala
CCT 192	GAA	CTC	CTG	GGG	GGA	CCG	TCA	GTC	TTC	CTC	TTC	CCC	CCA	AAA	CCC
Pro	Glu	Leu 25	Leu	Gly	Gly	Pro	Ser 30	Val	Phe	Leu	Phe	Pro 35	Pro	Lys	Pro
AAG 240	GAC	ACC	CTC	ATG	ATC	TCC	CGG	ACC	CCT	GAG	GTC	ACA	TGC	GTG	GTG
Lys	Asp 40	Thr	Leu	Met	Ile	Ser 45	Arg	Thr	Pro	Glu	Val 50	Thr	Cys	Val	Val
GTG 288	GAC	GTG	AGC	CAC	GAA	GAC	CCT	GAG	GTC	AAG	TTC	AAC	TGG	TAC	GTG
Val 55	Asp	Val	Ser	His	Glu 60	Asp	Pro	Glu	Val	Lys 65	Phe	Asn	Trp	Tyr	Val 70
GAC 336	GGC	GTG	GAG	GTG	CAT	AAT	GCC	AAG	ACA	AAG	CCG	CGG	GAG	GAG	CAG
Asp	Gly	Val	Glu	Val 75	His	Asn	Ala	Lys	Thr 80	Lys	Pro	Arg	Glu	Glu 85	Gln
TAC 384	AAC	AGC	ACG	TAC	CGG	GTG	GTC	AGC	GTC	CTC	ACC	GTC	CTG	CAC	CAG
Tyr	Asn	Ser	Thr 90	Tyr	Arg	Val	Val	Ser 95	Val	Leu	Thr	Val	Leu 100	His	Gln
GAC 432	TGG	CTG	AAT	GGC	AAG	GAG	TAC	AAG	TGC	AAG	GTC	TCC	AAC	AAA	GCC
Asp	Trp	Leu 105	Asn	Gly	Lys	Glu	Tyr 110	Lys	Cys	Lys	Val	Ser 115	Asn	Lys	Ala
CTC 480	CCA	GCC	CCC	ATC	GAG	AAA	ACC	ATC	TCC	AAA	GCC	AAA	GGG	CAG	CCC
Leu	Pro 120	Ala	Pro	Ile	Glu	Lys 125	Thr	Ile	Ser	Lys	Ala 130	Lys	Gly	Gln	Pro
CGA 528	GAA	CCA	CAG	GTG	TAC	ACC	CTG	CCC	CCA	TCC	CGG	GAT	GAG	CTG	ACC
Arg 135	Glu	Pro	Gln	Val	Tyr 140	Thr	Leu	Pro	Pro	Ser 145	Arg	Asp	Glu	Leu	Thr 150

AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC  
 576  
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
 155 160 165

GAC ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC  
 624  
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr  
 170 175 180

AAG ACC ACG CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC  
 672  
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr  
 185 190 195

AGC AAG CTC ACC GTG GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC  
 720  
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  
 200 205 210

TCA TGC TCC GTG ATG CAT GGT GGC GGA GGG TCA GGC GGA GGT GGG TCC  
 768  
 Ser Cys Ser Val Met His Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
 215 220 225 230

GGA GGC GGG GGT TCA AGT TCT GAC AAG ATA GAA GAT GAA AGG AAT CTT  
 816  
 Gly Gly Gly Gly Ser Ser Ser Asp Lys Ile Glu Asp Glu Arg Asn Leu  
 235 240 245

CAT GAA GAT TTT GTA TTC ATG AAA ACG ATA CAG AGA TGC AAC ACA GGA  
 864  
 His Glu Asp Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly  
 250 255 260

GAA AGA TCC TTA TCC TTA CTG AAC TGT GAG GAG ATT AAA AGC CAG TTT  
 912  
 Glu Arg Ser Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe  
 265 270 275

GAA GGC TTT GTG AAG GAT ATA ATG TTA AAC AAA GAG GAG ACG AAG AAA  
 960  
 Glu Gly Phe Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys  
 280 285 290

GAA AAC AGC TTT GAA ATG CAA AAA GGT GAT CAG AAT CCT CAA ATT GCG  
 1008  
 Glu Asn Ser Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala  
 295 300 305 310

GCA CAT GTC ATA AGT GAG GCC AGC AGT AAA ACA ACA TCT GTG TTA CAG  
 1056  
 Ala His Val Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln  
 315 320 325

TGG GCT GAA AAA GGA TAC TAC ACC ATG AGC AAC AAC TTG GTA ACC CTG  
 1104  
 Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu

576  
 624  
 672  
 720  
 768  
 816  
 864  
 912  
 960  
 1008  
 1056  
 1104

330

335

340

GAA AAT GGG AAA CAG CTG ACC GTT AAA AGA CAA GGA CTC TAT TAT ATC  
1152

Glu Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile  
345 350 355

TAT GCC CAA GTC ACC TTC TGT TCC AAT CGG GAA GCT TCG AGT CAA GCT  
1200

Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala  
360 365 370

CCA TTT ATA GCC AGC CTC TGC CTA AAG TCC CCC GGT AGA TTC GAG AGA  
1248

Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg  
375 380 385 390

ATC TTA CTC AGA GCT GCA AAT ACC CAC AGT TCC GCC AAA CCT TGC GGG  
1296

Ile Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly  
395 400 405

CAA CAA TCC ATT CAC TTG GGA GGA GTA TTT GAA TTG CAA CCA GGT GCT  
1344

Gln Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala  
410 415 420

TCG GTG TTT GTC AAT GTG ACT GAT CCA AGC CAA GTG AGC CAT GGC ACT  
1392

Ser Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr  
425 430 435

GGC TTC ACG TCC TTT GGC TTA CTC AAA CTC TGA  
1425

Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu  
440 445

## (2) INFORMATION FOR SEQ ID NO:16:

### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

### (ii) MOLECULE TYPE: protein

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile  
-25 -20 -15 -10

Leu Val Leu Leu Pro Val Thr Ser Ser Asp Tyr Lys Asp Asp Asp Asp  
-5 1 5

Lys Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro  
10 15 20



[illegible]

330

335

340

Asn Gly Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr  
 345 350 355

Ala Gln Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro  
 360 365 370 375

Phe Ile Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile  
 380 385 390

Leu Leu Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln  
 395 400 405

Gln Ser Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser  
 410 415 420

Val Phe Val Asn Val Thr Asp Pro Ser Gln Val Ser His Gly Thr Gly  
 425 430 435

Phe Thr Ser Phe Gly Leu Leu Lys Leu  
 440 445

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Arg Met Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile  
 1 5 10 15

Tyr His Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu  
 20 25 30

Arg

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 55 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATATGAATTC GACTACAAAG ATGACGATGA TAAACCTCAA ATTGCAGCAC ACGTT  
21

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTTCGCGGC CGCGTTCAGA GTTTGAGTAA GCCAA  
35

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 929 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:  
    (A) ORGANISM: Human CD40-L trimer

(ix) FEATURE:  
    (A) NAME/KEY: sig\_peptide  
    (B) LOCATION: 65..142

(ix) FEATURE:  
    (A) NAME/KEY: CDS  
    (B) LOCATION: 65..886

(ix) FEATURE:  
    (A) NAME/KEY: mat\_peptide  
    (B) LOCATION: 143..886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGAGCGAGTC CGCATCGACG GATCGGAAAA CCTCTCCGAG GTACCTATCC CGGGGATCCC

CACC ATG TTC CAT GTT TCT TTT AGA TAT ATC TTT GGA ATT CCT CCA CTG	109
Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu	
-26 -25 -20 -15	
ATC CTT GTT CTG CTG CCT GTC ACT AGT TCT GAC CGT ATG AAA CAG ATA	157
Ile Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met Lys Gln Ile	
-10 -5 1 5	
GAG GAT AAG ATC GAA GAG ATC CTA AGT AAG ATT TAT CAT ATA GAG AAT	205
Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn	
10 15 20	
GAA ATC GCC CGT ATC AAA AAG CTG ATT GGC GAG CGG ACT AGT TCT GAC	253
Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Ser Ser Asp	
25 30 35	
AAG ATA GAA GAT GAA AGG AAT CTT CAT GAA GAT TTT GTA TTC ATG AAA	301
Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys	
40 45 50	
ACG ATA CAG AGA TGC AAC ACA GGA GAA AGA TCC TTA TCC TTA CTG AAC	349
Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser Leu Leu Asn	
55 60 65	
TGT GAG GAG ATT AAA AGC CAG TTT GAA GGC TTT GTG AAG GAT ATA ATG	397
Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met	
70 75 80 85	
TTA AAC AAA GAG GAG ACG AAG AAA GAA AAC AGC TTT GAA ATG CAA AAA	445
Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser Phe Glu Met Gln Lys	
90 95 100	
GGT GAT CAG AAT CCT CAA ATT GCG GCA CAT GTC ATA AGT GAG GCC AGC	493
Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser	
105 110 115	
AGT AAA ACA ACA TCT GTG TTA CAG TGG GCT GAA AAA GGA TAC TAC ACC	541
Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr	
120 125 130	
ATG AGC AAC AAC TTG GTA ACC CTG GAA AAT GGG AAA CAG CTG ACC GTT	589
Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val	
135 140 145	
AAA AGA CAA GGA CTC TAT TAT ATC TAT GCC CAA GTC ACC TTC TGT TCC	637
Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser	
150 155 160 165	
AAT CGG GAA GCT TCG AGT CAA GCT CCA TTT ATA GCC AGC CTC TGC CTA	685
Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu	
170 175 180	
AAG TCC CCC GGT AGA TTC GAG AGA ATC TTA CTC AGA GCT GCA AAT ACC	733
Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr	
185 190 195	
CAC AGT TCC GCC AAA CCT TGC GGG CAA CAA TCC ATT CAC TTG GGA GGA	781

66356: TGGGGG

His	Ser	Ser	Ala	Lys	Pro	Cys	Gly	Gln	Gln	Ser	Ile	His	Leu	Gly	Gly	
		200					205					210				
GTA	TTT	GAA	TTG	CAA	CCA	GGT	GCT	TCG	GTG	TTT	GTC	AAT	GTG	ACT	GAT	829
Val	Phe	Glu	Leu	Gln	Pro	Gly	Ala	Ser	Val	Phe	Val	Asn	Val	Thr	Asp	
	215					220					225					
CCA	AGC	CAA	GTG	AGC	CAT	GGC	ACT	GGC	TTC	ACG	TCC	TTT	GGC	TTA	CTC	877
Pro	Ser	Gln	Val	Ser	His	Gly	Thr	Gly	Phe	Thr	Ser	Phe	Gly	Leu	Leu	
230					235					240				245		
AAA	CTC	TGAGCGGCCG	CTACAGATGA	ATAATAAGCA	TGTTTGGATT	CCTCAA										929
Lys	Leu															

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Phe	His	Val	Ser	Phe	Arg	Tyr	Ile	Phe	Gly	Ile	Pro	Pro	Leu	Ile	
-26	-25					-20				-15						
Leu	Val	Leu	Leu	Pro	Val	Thr	Ser	Ser	Asp	Arg	Met	Lys	Gln	Ile	Glu	
-10				-5						1				5		
Asp	Lys	Ile	Glu	Glu	Ile	Leu	Ser	Lys	Ile	Tyr	His	Ile	Glu	Asn	Glu	
			10					15					20			
Ile	Ala	Arg	Ile	Lys	Lys	Leu	Ile	Gly	Glu	Arg	Thr	Ser	Ser	Asp	Lys	
		25					30					35				
Ile	Glu	Asp	Glu	Arg	Asn	Leu	His	Glu	Asp	Phe	Val	Phe	Met	Lys	Thr	
	40					45					50					
Ile	Gln	Arg	Cys	Asn	Thr	Gly	Glu	Arg	Ser	Leu	Ser	Leu	Leu	Asn	Cys	
55					60					65				70		
Glu	Glu	Ile	Lys	Ser	Gln	Phe	Glu	Gly	Phe	Val	Lys	Asp	Ile	Met	Leu	
				75					80					85		
Asn	Lys	Glu	Glu	Thr	Lys	Lys	Glu	Asn	Ser	Phe	Glu	Met	Gln	Lys	Gly	
			90					95					100			
Asp	Gln	Asn	Pro	Gln	Ile	Ala	Ala	His	Val	Ile	Ser	Glu	Ala	Ser	Ser	
		105				110						115				
Lys	Thr	Thr	Ser	Val	Leu	Gln	Trp	Ala	Glu	Lys	Gly	Tyr	Tyr	Thr	Met	
	120					125					130					
Ser	Asn	Asn	Leu	Val	Thr	Leu	Glu	Asn	Gly	Lys	Gln	Leu	Thr	Val	Lys	

135		140		145		150									
Arg	Gln	Gly	Leu	Tyr	Tyr	Ile	Tyr	Ala	Gln	Val	Thr	Phe	Cys	Ser	Asn
				155					160					165	
Arg	Glu	Ala	Ser	Ser	Gln	Ala	Pro	Phe	Ile	Ala	Ser	Leu	Cys	Leu	Lys
			170					175					180		
Ser	Pro	Gly	Arg	Phe	Glu	Arg	Ile	Leu	Leu	Arg	Ala	Ala	Asn	Thr	His
		185					190					195			
Ser	Ser	Ala	Lys	Pro	Cys	Gly	Gln	Gln	Ser	Ile	His	Leu	Gly	Gly	Val
	200					205					210				
Phe	Glu	Leu	Gln	Pro	Gly	Ala	Ser	Val	Phe	Val	Asn	Val	Thr	Asp	Pro
215				220						225					230
Ser	Gln	Val	Ser	His	Gly	Thr	Gly	Phe	Thr	Ser	Phe	Gly	Leu	Leu	Lys
				235					240					245	

Leu

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 878 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
  - (B) CLONE: Murine CD40-L trimer
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: 15..92
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 15..857
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 93..857

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCGAGGTAC	CGCC	ATG	TTC	CAT	GTT	TCT	TTT	AGA	TAT	ATC	TTT	GGA	ATT	50	
		Met	Phe	His	Val	Ser	Phe	Arg	Tyr	Ile	Phe	Gly	Ile		
		-26	-25					-20				-15			
CCT	CCA	CTG	ATC	CTT	GTT	CTG	CTG	CCT	GTC	ACT	AGT	TCT	GAC	CGT	ATG
Pro	Pro	Leu	Ile	Leu	Val	Leu	Leu	Pro	Val	Thr	Ser	Ser	Asp	Arg	Met
				-10				-5						1	98

AAA Lys	CAG Gln	ATA Ile	GAG Glu	GAT Asp	AAG Lys	ATC Ile	GAA Glu	GAG Glu	ATC Ile	CTA Leu	AGT Ser	AAG Lys	ATT Ile	TAT Tyr	CAT His	146
5 10 15																
ATA Ile	GAG Glu	AAT Asn	GAA Glu	ATC Ile	GCC Ala	CGT Arg	ATC Ile	AAA Lys	AAG Lys	CTG Leu	ATT Ile	GGC Gly	GAG Glu	CGG Arg	ACT Thr	194
20 25 30																
AGT Ser	TCT Ser	GAC Asp	TAC Tyr	AAA Lys	GAT Asp	GAC Asp	GAT Asp	GAT Asp	AAA Lys	GAT Asp	AAG Lys	GTC Val	GAA Glu	GAG Glu	GAA Glu	242
35 40 45 50																
GTA Val	AAC Asn	CTT Leu	CAT His	GAA Glu	GAT Asp	TTT Phe	GTA Val	TTC Phe	ATA Ile	AAA Lys	AAG Lys	CTA Leu	AAG Lys	AGA Arg	TGC Cys	290
55 60 65																
AAC Asn	AAA Lys	GGA Gly	GAA Glu	GGA Gly	TCT Ser	TTA Leu	TCC Ser	TTG Leu	CTG Leu	AAC Asn	TGT Cys	GAG Glu	GAG Glu	ATG Met	AGA Arg	338
70 75 80																
AGG Arg	CAA Gln	TTT Phe	GAA Glu	GAC Asp	CTT Leu	GTC Val	AAG Lys	GAT Asp	ATA Ile	ACG Thr	TTA Leu	AAC Asn	AAA Lys	GAA Glu	GAG Glu	386
85 90 95																
AAA Lys	AAA Lys	GAA Glu	AAC Asn	AGC Ser	TTT Phe	GAA Glu	ATG Met	CAA Gln	AGA Arg	GGT Gly	GAT Asp	GAG Glu	GAT Asp	CCT Pro	CAA Gln	434
100 105 110																
ATT Ile	GCA Ala	GCA Ala	CAC His	GTT Val	GTA Val	AGC Ser	GAA Glu	GCC Ala	AAC Asn	AGT Ser	AAT Asn	GCA Ala	GCA Ala	TCC Ser	GTT Val	482
115 120 125 130																
CTA Leu	CAG Gln	TGG Trp	GCC Ala	AAG Lys	AAA Lys	GGA Gly	TAT Tyr	TAT Tyr	ACC Thr	ATG Met	AAA Lys	AGC Ser	AAC Asn	TTG Leu	GTA Val	530
135 140 145																
ATG Met	CTT Leu	GAA Glu	AAT Asn	GGG Gly	AAA Lys	CAG Gln	CTG Leu	ACG Thr	GTT Val	AAA Lys	AGA Arg	GAA Glu	GGA Gly	CTC Leu	TAT Tyr	578
150 155 160																
TAT Tyr	GTC Val	TAC Tyr	ACT Thr	CAA Gln	GTC Val	ACC Thr	TTC Phe	TGC Cys	TCT Ser	AAT Asn	CGG Arg	GAG Glu	CCT Pro	TCG Ser	AGT Ser	626
165 170 175																
CAA Gln	CGC Arg	CCA Pro	TTC Phe	ATC Ile	GTC Val	GGC Gly	CTC Leu	TGG Trp	CTG Leu	AAG Lys	CCC Pro	AGC Ser	AGT Ser	GGA Gly	TCT Ser	674
180 185 190																
GAG Glu	AGA Arg	ATC Ile	TTA Leu	CTC Leu	AAG Lys	GCG Ala	GCA Ala	AAT Asn	ACC Thr	CAC His	AGT Ser	TCC Ser	TCC Ser	CAG Gln	CTT Leu	722
195 200 205 210																
TGC Cys	GAG Glu	CAG Gln	CAG Gln	TCT Ser	GTT Val	CAC His	TTG Leu	GGC Gly	GGA Gly	GTG Val	TTT Phe	GAA Glu	TTA Leu	CAA Gln	GCT Ala	770
215 220 225																
GGT Gly	GCT Gly	TCT Gly	GTG Gly	TTT Gly	GTC Gly	AAC Gly	GTG Gly	ACT Gly	GAA Gly	GCA Gly	AGC Gly	CAA Gly	GTG Gly	ATC Gly	CAC Gly	818

Gly Ala Ser Val Phe Val Asn Val Thr Glu Ala Ser Gln Val Ile His  
 230 235 240

AGA GTT GGC TTC TCA TCT TTT GGC TTA CTC AAA CTC TGAACGCGGC  
 Arg Val Gly Phe Ser Ser Phe Gly Leu Leu Lys Leu  
 245 250 255

864

CGCTACAGAT CTAC

878

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile  
 -26 -25 -20 -15

Leu Val Leu Leu Pro Val Thr Ser Ser Asp Arg Met Lys Gln Ile Glu  
 -10 -5 1 5

Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu Asn Glu  
 10 15 20

Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Ser Ser Asp Tyr  
 25 30 35

Lys Asp Asp Asp Asp Lys Asp Lys Val Glu Glu Glu Val Asn Leu His  
 40 45 50

Glu Asp Phe Val Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu  
 55 60 65 70

Gly Ser Leu Ser Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu  
 75 80 85

Asp Leu Val Lys Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn  
 90 95 100

Ser Phe Glu Met Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His  
 105 110 115

Val Val Ser Glu Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala  
 120 125 130

Lys Lys Gly Tyr Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn  
 135 140 145 150

Gly Lys Gln Leu Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr  
 155 160 165

Gln Val Thr Phe Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe



170

175

180

Ile Val Gly Leu Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu  
185 190 195

Leu Lys Ala Ala Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln  
200 205 210

Ser Val His Leu Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val  
215 220 225 230

Phe Val Asn Val Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe  
235 240 245

Ser Ser Phe Gly Leu Leu Lys Leu  
250

170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250